

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:21:54 ; Search time 45.33 Seconds

(without alignments)  
178,061 Million cell updates/sec

Title: US-09-351-778a-12

Sequence: 84 MGGSTAPTYDYRNTATG.....NEKIRHLDGKRCSSLLQYD 84

Scoring table: OLIGO  
Gapop 60.0 , Capext 60.0

Searched: 283138 segs, 96089334 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR.71.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	22.6	93	1	ERAD53
2	7	8.3	160	2	C95415
3	7	8.3	193	2	hypothetical prote
4	7	8.3	197	2	probable sideroph
5	7	8.3	387	2	C86523
6	7	8.3	391	2	C89783
7	7	8.3	425	2	D97201
8	7	8.3	459	2	AC9909
9	7	8.3	487	2	C87534
10	7	8.3	495	2	B97684
11	7	8.3	495	2	H71933
12	7	8.3	536	2	D44578
13	7	8.3	891	2	T36423
14	7	8.3	1175	2	T36423
15	7	8.3	82	2	hypothetical prote
16	7	8.3	83	2	D82630
17	7	8.3	89	2	D87338
18	7	8.3	89	2	D87338
19	7	8.3	94	2	E82629
20	7	8.3	94	2	D82626
21	7	8.3	97	2	I79265
22	7	8.3	97	2	T40639
23	7	8.3	113	2	C81230
24	7	8.3	113	2	G81990
25	7	8.3	115	2	B64637
26	7	8.3	119	2	H83186
27	7	8.3	121	1	U01646
28	7	8.3	126	1	D95915
29	7	8.3	130	2	E70353
30	7	8.3	131	2	T25687

30	6	7.1	134	2	S52546	Uthionin variant Th
31	6	7.1	136	2	T23996	hypothetical prote
32	6	7.1	142	2	S32960	hypothetical prote
33	6	7.1	144	2	AE3588	high-affinity bran
34	6	7.1	148	2	T03569	hypothetical 16.9k
35	6	7.1	149	2	AG2708	conserved hypothet
36	6	7.1	150	2	G87270	general secretion
37	6	7.1	151	2	D64319	probable formate d
38	6	7.1	157	2	S75191	hypothetical prote
39	6	7.1	157	2	S35037	helix-loop-helix p
40	6	7.1	157	2	T46883	hypothetical prote
41	6	7.1	160	2	D83575	hypothetical prote
42	6	7.1	170	2	T17286	hypothetical prote
43	6	7.1	172	2	F83337	probable sigma-70
44	6	7.1	174	2	T21945	hypothetical prote
45	6	7.1	177	2	F87600	conserved hypothet

#### ALIGNMENTS

RESULT 1  
ERAD53  
early E3A 10.5K prote in - human adenovirus 5  
C:Species: Mastadenovirus h5 (human adenovirus 5)  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 16-Jul-1999  
C:Accession: A05245  
R:Cladarias, C.; Mold, W.S.M.  
Virology 140, 28-43, 1985  
A>Title: DNA sequence of the early E3 transcription unit of adenovirus 5.  
A:Reference number: A94335; MUID:85092388  
A:Accession: A05245  
A:Molecule type: DNA  
A:Residues: 1-93 <CLN>  
A:Cross-References: GB:X03002; NID:958503; PIDN:CA26784.1; PID:958507  
C:Superfamily: adenovirus early E3A 10.5K protein  
C:Keywords: early protein; transmembrane protein

Query Match 22.68; Score 19; DB 1; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 IALMFVCLIIIMLICLK 47  
DB 39 IALMFVCLIIIMLICLK 57

#### RESULT 2

C95415  
hypothetical protein SMA2279 (imported) - Sinorhizobium meliloti (strain 1021) magap1  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: C95415  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: C95415  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-160 <CUR>  
A:Cross-References: GB:AE006469; PIDN:AAK65885.1; PID:914524394; GSPDB:GN00165  
A:Experimental source: strain 1021, megaplasmid pSymA  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl  
P.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau  
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,  
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma2279  
A:Genome: plasmid

Query Match 8.3%; Score 7; DB 2; Length 160;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8  
Db 28 TGSTIAP 34

RESULT 3  
AC0186  
probable siderophore biosynthetic enzyme a1CB [Imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AC0186  
R:Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Ruthford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Status: preliminary  
A:Accession: AC0186  
A:Residues: 1-193 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CMC90354.1; PID:q15979574; GSPDB:GN00175  
C:Genetics:  
A:Gene: a1CB

Query Match 8.3%; Score 7; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 65 NEKHRL 71  
Db 149 NEKHRL 155

RESULT 4  
C86523  
CT142 hypothetical protein\_2 [Imported] - Chlamydomonas pneumoniae (strain J138)  
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001  
C:Accession: C86523  
R:Shirai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
A:Reference number: AB4491; MUID:20330349  
A:Accession: C86523  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-197 <STO>  
A:Cross-references: GB:BA000008; MUID:98978632; PIDN:BAA98469.1; GSPDB:GN00142  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: CPJ0259

Query Match 8.3%; Score 7; DB 2; Length 197;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23  
Db 74 ATGLTSA 80

RESULT 5  
C89783  
hypothetical protein SA0200 [Imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
C:Accession: C89783  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O  
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.  
C.; Shiba, T.; Hattori, M.; Ogatawara, N.; Hayashi, H.; Hiratsuki, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: AB9758; MUID:21311952; PMID:11418146  
A:Accession: C89783  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-387 <KUR>  
A:Cross-references: GB:BA000018; PID:q13700123; PIDN:BBB41422.1; GSPDB:GN00149  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA0200

Query Match 8.3%; Score 7; DB 2; Length 387;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LTSALNL 26  
Db 27 LTSALNL 33

RESULT 6  
D97201  
a1CAR transformylase domain of PurH-like protein [Imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: D97201  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: AB96900; MUID:21359325; PMID:21359325  
A:Accession: D97201  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-391 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK80399.1; PID:q15025462; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CMC2445

Query Match 8.3%; Score 7; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23  
Db 58 ATGLTSA 64

RESULT 7  
AC2909  
MFS permease [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
C:Accession: AC2909  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; MCCI  
Science 294, 2317-2323, 2001

A:Author: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
 A:Reference number: AB2577; PMID:11743193  
 A:Accession: AC2909  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-425 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AA143689.1; PID:917741216; GSPDB:GN00186  
 A:Experimental source: strain C58 (DuPont)  
 C:Genetics:  
 A:Gene: Atu2708  
 A:Map position: circular chromosome

Query Match 8.3%; Score 7; DB 2; Length 425;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 TGSTAP 8  
 DB 390 TGSTAP 396

RESULT 8  
 C87534  
 hypothetical protein CC2300 [imported] - *Caulobacter crescentus*  
 C:Species: *Caulobacter crescentus*  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C:Accession: C87534  
 R:Name: W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 n, J.; Land, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolon  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A:Reference number: A87249; MUID:21173698; PMID:11259647  
 A:Accession: C87534  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-459 <STO>  
 A:Cross-references: GB:AE005673; NID:g13423819; PIDN:AAK24271.1; GSPDB:GN00148  
 C:Genetics:  
 A:Gene: CC2300  
 C:Superfamily: Arabidopsis 2-dehydro-3-deoxyheptonate aldolase 1

Query Match 8.3%; Score 7; DB 2; Length 459;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 60 VLNPHE 66  
 DB 308 VLNPHE 314

RESULT 9  
 B97684  
 Probable taurate transporter AGR\_C4908 [imported] - *Agrobacterium tumefaciens* (strain  
 C:Species: *Agrobacterium tumefaciens*  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
 C:Accession: B97684  
 R:Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
 Science 294, 2323-2328, 2001  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*  
 A:Reference number: A97359; PMID:11743194  
 A:Accession: B97684  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-487 <KUR>  
 A:Cross-references: GB:AE007869; PIDN:AAK8427.1; PID:g15157922; GSPDB:GN00169  
 C:Genetics:  
 A:Gene: AGR\_C4908

A:Map position: circular chromosome

Query Match 8.3%; Score 7; DB 2; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 TGSTAP 8  
 DB 452 TGSTAP 458

RESULT 10  
 H71933  
 hypothetical protein jhp0420 - *Helicobacter pylori* (strain J99)  
 C:Species: *Helicobacter pylori*  
 A:Variety: strain J99  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 28-Jul-2000  
 C:Accession: H71933  
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.  
 i Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F  
 Nature 397, 176-180, 1999  
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p  
 A:Reference number: A71800; MUID:99120557  
 A:Accession: H71933  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-495 <ARN>  
 A:Cross-references: GB:AE001476; GB:AE001439; NID:g4154949; PIDN:AAD06001.1; PID:g4415  
 C:Genetics:  
 A:Gene: jhp0420  
 C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0420

Query Match 8.3%; Score 7; DB 2; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 26 LPOTALM 32  
 DB 467 LPOTALM 473

RESULT 11  
 D64578  
 conserved hypothetical protein HP0468 - *Helicobacter pylori* (strain 26695)  
 C:Species: *Helicobacter pylori*  
 C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 28-Jul-2000  
 C:Accession: D64578  
 R:Tomb, J.F.; White, O.; Krlavag, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKe  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney,  
 Nature 388, 539-547, 1997  
 A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
 A:Reference number: A64520; MUID:97394467  
 A:Accession: D64578  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-495 <TOM>  
 A:Cross-references: GB:AE000561; GB:AE000511; NID:g2313564; PIDN:AAD07530.1; PID:g231  
 C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0420

Query Match 8.3%; Score 7; DB 2; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 26 LPOTALM 32  
 DB 467 LPOTALM 473

## RESULT 12

T27668

hypothetical protein ZK1053.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000

C:Accession: T27668

R:Kershaw, J.

Submitted to the EMBL Data Library, November 1996

A:Reference number: Z20402

A:Accession: T27668

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-536 &lt;WIL&gt;

A:Cross-references: EMBL:Z82084; PIDN:CA804976.1; GSPDB:GN00019; CESP:ZK1053.2

A:Experimental source: clone ZK1053

C:Genetics:

A:Gene: CESP:ZK1053.2

A:Map position: 1

A:Introns: 56/3; 88/3; 203/1; 228/2; 383/1; 467/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZK1053.2

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 536;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 STIAPTT 10

DB 295 STIAPTT 301

## RESULT 13

T36423

probable large, multifunctional secreted protein - *Streptomyces coelicolor* (fragment)C:Species: *Streptomyces coelicolor*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T36423

R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, September 1999

A:Reference number: Z21606

A:Accession: T36423

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-891 &lt;SAU&gt;

A:Cross-references: EMBL:AL10974; PIDN:CA853335.1; GSPDB:GN00070; SCOEDB:SCF34.24

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCF34.24

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 891;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 RLDGLKP 76

DB 628 RLDGLKP 634

## RESULT 14

H83437

hypothetical protein PA1669 [imported] - *Pseudomonas aeruginosa* (strain PA01)C:Species: *Pseudomonas aeruginosa*

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: H83437

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.D.; Br

adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laribay, K.; Llm,

Nature 406: 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: H83437

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1175 <STO>

A:Cross-references: GB:AE004594; GB:AE004091; NID:g9947630; PIDN:MAC05058.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1669

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 1175;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 KRRARP 52

DB 213 KRRARP 219

## RESULT 15

D82630

hypothetical protein XF1852 [imported] - *Xylella fastidiosa* (strain 9a5c)C:Species: *Xylella fastidiosa*

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: D82630

R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq

Nature 406: 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82630

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-82 &lt;SIM&gt;

A:Cross-references: GB:AE004006; GB:AE003849; NID:g9106932; PIDN:AF84658.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre

as-Neto, E.; Docena, C.; El-dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kurame, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.C.R.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1852

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 82;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 KPCLSL 80

DB 32 KPCLSL 37

Search completed: June 21, 2002, 08:21:55

Job time: 100 sec

